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List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9788049/publications.pdf>

Version: 2024-02-01

14
papers

39,626
citations

623574

14
h-index

996849

15
g-index

17
all docs

17
docs citations

17
times ranked

60686
citing authors

#	ARTICLE	IF	CITATIONS
1	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , 2019, 47, D607-D613.	6.5	12,237
2	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	6.5	9,029
3	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , 2017, 45, D362-D368.	6.5	6,303
4	The STRING database in 2021: customizable protein-protein networks, and functional characterization of user-uploaded gene/measurement sets. <i>Nucleic Acids Research</i> , 2021, 49, D605-D612.	6.5	4,274
5	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , 2019, 47, D309-D314.	6.5	2,575
6	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017, 34, 2115-2122.	3.5	2,156
7	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016, 44, D286-D293.	6.5	1,937
8	Version 4.0 of PaxDb: Protein abundance data, integrated across model organisms, tissues, and cell-lines. <i>Proteomics</i> , 2015, 15, 3163-3168.	1.3	493
9	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	198
10	GUNC: detection of chimerism and contamination in prokaryotic genomes. <i>Genome Biology</i> , 2021, 22, 178.	3.8	94
11	WeGET: predicting new genes for molecular systems by weighted co-expression. <i>Nucleic Acids Research</i> , 2016, 44, D567-D573.	6.5	35
12	Analysis of the Human Kinome and Phosphatome by Mass Cytometry Reveals Overexpression-Induced Effects on Cancer-Related Signaling. <i>Molecular Cell</i> , 2019, 74, 1086-1102.e5.	4.5	32
13	Pathogenic impact of transcript isoform switching in 1,209 cancer samples covering 27 cancer types using an isoform-specific interaction network. <i>Scientific Reports</i> , 2020, 10, 14453.	1.6	27
14	Tree reconciliation combined with subsampling improves large scale inference of orthologous group hierarchies. <i>BMC Bioinformatics</i> , 2019, 20, 228.	1.2	1